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## RAW SEQUENCE LISTING

DATE: 10/08/2002 p.6  
TIME: 13:44:35

PATENT APPLICATION: US/09/757,415A

Input Set : A:\2459-002N.ST25.txt

Output Set: N:\CRF4\10082002\I757415A.raw

2 <110> APPLICANT: Zhou, Ming-Ming  
 4 <120> TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor  
 6 <130> FILE REFERENCE: 2459-1-002N  
 8 <140> CURRENT APPLICATION NUMBER: 09/757415A  
 9 <141> CURRENT FILING DATE: 2001-01-09  
 11 <150> PRIOR APPLICATION NUMBER: 60/175867  
 12 <151> PRIOR FILING DATE: 2000-01-12  
 14 <160> NUMBER OF SEQ ID NOS: 7  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 508  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Homo sapien  
 23 <400> SEQUENCE: 1  
 25 Met Gly Ser Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn  
 26 1 5 10 15  
 29 His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu  
 30 20 25 30  
 33 Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr  
 34 35 40 45  
 37 Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg  
 38 50 55 60  
 41 Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys  
 42 65 70 75 80  
 45 Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu  
 46 85 90 95  
 49 Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val  
 50 100 105 110  
 53 Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu  
 54 115 120 125  
 57 Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln  
 58 130 135 140  
 61 Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser  
 62 145 150 155 160  
 65 Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro  
 66 165 170 175  
 69 Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln  
 70 180 185 190  
 73 Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn  
 74 195 200 205  
 77 Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu  
 78 210 215 220  
 81 Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro

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```

82 225                230                235                240
85 Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr
86                245                250                255
89 Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly
90                260                265                270
93 Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr
94                275                280                285
97 Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu
98                290                295                300
101 Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val
102 305                310                315                320
105 Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile
106                325                330                335
109 Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu
110                340                345                350
113 Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu
114                355                360                365
117 Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn
118                370                375                380
121 Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val
122 385                390                395                400
125 Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
126                405                410                415
129 Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
130                420                425                430
133 Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
134                435                440                445
137 Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
138                450                455                460
141 Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
142 465                470                475                480
145 Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
146                485                490                495
149 Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
150                500                505
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 822
155 <212> TYPE: PRT
156 <213> ORGANISM: Mus musculus
158 <400> SEQUENCE: 2
160 Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
161 1                5                10                15
164 Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
165                20                25                30
168 Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
169                35                40                45
172 Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
173                50                55                60
176 Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg

```

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```

177 65          70          75          80
180 Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
181          85          90          95
184 Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
185          100          105          110
188 Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
189          115          120          125
192 Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
193          130          135          140
196 Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
197 145          150          155          160
200 Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
201          165          170          175
204 Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
205          180          185          190
208 Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
209          195          200          205
212 Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
213          210          215          220
216 Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
217 225          230          235          240
220 His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
221          245          250          255
224 Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn
225          260          265          270
228 Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
229          275          280          285
232 Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
233          290          295          300
236 Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
237 305          310          315          320
240 Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
241          325          330          335
244 Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
245          340          345          350
248 Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
249          355          360          365
252 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
253          370          375          380
256 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys
257 385          390          395          400
260 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
261          405          410          415
264 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
265          420          425          430
268 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
269          435          440          445
272 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu
273          450          455          460

```

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Output Set: N:\CRF4\10082002\I757415A.raw

```

276 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
277 465                               470                               475                               480
280 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
281                               485                               490                               495
284 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
285                               500                               505                               510
288 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
289                               515                               520                               525
292 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
293                               530                               535                               540
296 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
297 545                               550                               555                               560
300 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
301                               565                               570                               575
304 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
305                               580                               585                               590
308 Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
309                               595                               600                               605
312 Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
313                               610                               615                               620
316 Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
317 625                               630                               635                               640
320 Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
321                               645                               650                               655
324 Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
325                               660                               665                               670
328 Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
329                               675                               680                               685
332 Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
333                               690                               695                               700
336 Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
337 705                               710                               715                               720
340 Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
341                               725                               730                               735
344 Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
345                               740                               745                               750
348 Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp
349                               755                               760                               765
352 Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
353                               770                               775                               780
356 Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
357 785                               790                               795                               800
360 Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn
361                               805                               810                               815
364 Ser Gly Leu Lys Arg Arg
365                               820
368 <210> SEQ ID NO: 3
369 <211> LENGTH: 22
370 <212> TYPE: PRT

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Input Set : A:\2459-002N.ST25.txt

Output Set: N:\CRF4\10082002\I757415A.raw

```

371 <213> ORGANISM: Mus musculus
373 <400> SEQUENCE: 3
375 His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg
376 1          5          10          15
378 Arg Gln Val Thr Val Ser
379          20
382 <210> SEQ ID NO: 4
383 <211> LENGTH: 11
384 <212> TYPE: PRT
385 <213> ORGANISM: Artificial Sequence
W--> 386 <220> FEATURE:
387 <223> OTHER INFORMATION: Tyrosine phosphorylation peptide
W--> 389 <220> FEATURE:
390 <221> NAME/KEY: MISC_FEATURE
391 <222> LOCATION: (9)..(9)
392 <223> OTHER INFORMATION: Xaa is a phosphotyrosine
394 <400> SEQUENCE: 4
W--> 396 Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser
397 1          5          10
400 <210> SEQ ID NO: 5
401 <211> LENGTH: 16
402 <212> TYPE: PRT
403 <213> ORGANISM: Artificial Sequence
W--> 404 <220> FEATURE:
405 <223> OTHER INFORMATION: Consensus sequence
W--> 407 <220> FEATURE:
408 <221> NAME/KEY: MISC_FEATURE
409 <222> LOCATION: (2)..(3)
410 <223> OTHER INFORMATION: Xaa can be any amino acid
W--> 412 <220> FEATURE:
413 <221> NAME/KEY: MISC_FEATURE
414 <222> LOCATION: (5)..(7)
415 <223> OTHER INFORMATION: Xaa can be any amino acid
W--> 417 <220> FEATURE:
418 <221> NAME/KEY: MISC_FEATURE
419 <222> LOCATION: (9)..(9)
420 <223> OTHER INFORMATION: Xaa can be any amino acid
W--> 422 <220> FEATURE:
423 <221> NAME/KEY: MISC_FEATURE
424 <222> LOCATION: (11)..(11)
425 <223> OTHER INFORMATION: Xaa can be any amino acid
W--> 427 <220> FEATURE:
428 <221> NAME/KEY: MISC_FEATURE
429 <222> LOCATION: (13)..(13)
430 <223> OTHER INFORMATION: Xaa can be any amino acid
W--> 432 <220> FEATURE:
433 <221> NAME/KEY: MISC_FEATURE
434 <222> LOCATION: (15)..(15)
435 <223> OTHER INFORMATION: Xaa can be any amino acid

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/757,415A

DATE: 10/08/2002  
TIME: 13:44:36

Input Set : A:\2459-002N.ST25.txt  
Output Set: N:\CRF4\10082002\I757415A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 9  
Seq#:5; Xaa Pos. 2,3,5,6,7,9,11,13,15  
Seq#:6; Xaa Pos. 3,4  
Seq#:7; Xaa Pos. 8

## VERIFICATION SUMMARY

DATE: 10/08/2002

PATENT APPLICATION: US/09/757,415A

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Input Set : A:\2459-002N.ST25.txt

Output Set: N:\CRF4\10082002\I757415A.raw

L:386 M:283 W: Missing Blank Line separator, <220> field identifier  
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:404 M:283 W: Missing Blank Line separator, <220> field identifier  
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:447 M:283 W: Missing Blank Line separator, <220> field identifier  
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:469 M:283 W: Missing Blank Line separator, <220> field identifier  
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0